

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 14, 2006, 01:34:23 ; Search time 75 Seconds
(without alignments)
3648.671 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEAGASQDDVSPFLRTS.....RLADNADHWAKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12295	78.1	5126	2	S40450
2	6828	43.4	5107	2	T29144
3	6770.5	43.0	4969	2	A37113
4	6769	43.0	4967	2	S72269
5	6534.5	41.5	5037	1	A54161
6	6453.5	41.0	5035	1	I46646
7	6442.5	40.9	5032	1	A35041
8	6439	40.9	5037	2	B35041
9	6438.5	40.9	4859	2	S74173
10	6423	40.8	4869	2	S66572
11	6419	40.8	4868	2	B54161
12	6413	40.7	4872	2	S27272
13	538	3.4	163	2	I47214
14	520	3.3	162	2	I47213
15	327	2.1	2783	2	T31431
16	323	2.1	2701	2	S17796
17	296.5	1.9	2693	2	A40743
18	292.5	1.9	2695	2	S54974
19	290.5	1.8	2670	2	A46719
20	289	1.8	2713	2	A55713
21	285	1.8	2671	2	A49873
22	285	1.8	2734	2	B36579
23	284	1.8	1966	2	T32552
24	284	1.8	2848	2	T32550
25	279	1.8	2749	1	A6M57T
26	279	1.8	2749	2	A36579
27	277.5	1.8	2833	2	A43360
28	205	1.3	1676	2	E71410
29	203.5	1.3	2541	2	T29340

30	198	1.3	3259	1	A56539	giantin - human
31	198	1.3	5369	2	T44807	myosubtilin synth
32	197.5	1.3	2954	2	T14156	myosin-related pr
33	196.5	1.2	2218	2	B84683	hypothetical prote
34	192	1.2	1727	2	T50073	myosin-like coiled
35	192	1.2	3225	2	I52300	giantin - human
36	191	1.2	1882	2	T00069	hypothetical prote
37	189.5	1.2	2663	1	S28261	centromere protein
38	188.5	1.2	1642	2	T08880	NMDA receptor-bind
39	188	1.2	4540	2	T30838	cytoplasmic dynein
40	182.5	1.2	2331	2	T25410	hypothetical prote
41	182.5	1.2	3187	2	J05837	36k Golgi complex
42	180.5	1.1	2712	2	T05113	hypothetical prote
43	179	1.1	6669	2	S55024	nebulin, skeletal
44	178	1.1	4151	2	T13734	groovin gene prote
45	177	1.1	52	2	I46644	ryanodine receptor

ALIGNMENTS

RESULT 1
S40450
ryanodine receptor/calcium release channel - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
C/Accession: S40450

R:Takehima, H.; Nishi, M.; Iwabe, N.; Miyata, T.; Hosoya, T.; Masai, I.; Hotta, Y.
FEBS Lett. 337, 81-87, 1994
A/Title: Isolation and characterization of a gene for a ryanodine receptor/calcium rel
A/Reference number: S40450; MUID:94102409; PMID:8276118
A/Accession: S40450
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-5126 <TRX>
A/Cross-references: UNIPARC:UP1000017CF36
C/Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 home

Query Match 78.1%; Score 12295; DB 2; Length 5126;
Best Local Similarity 77.5%; Pred. No. 0;
Matches 2348; Conservative 275; Mismatches 338; Indels 68; Gaps 22;

Qy	1	MAEAEAGASQDDVSPFLRTSDMVC	CTATGGRVCLAEFGNHCLENADNPDL	60
Db	1	MAEAEAG-SQDDVSPFLRTSDMTLS	CTATGGRVCLAEFGNHCLENADNPDL	59
Qy	61	SOCYFVIBOALSVBALOELVTAAGSE	FGKGTSGHRTLLGNALLRHNSDMYLA	120
Db	60	SOCYFVIBOALSVBALOELVTAAGSE	FGKGTSGHRTLLGNALLRHNSDMYLA	119
Qy	121	SSSQDKLAPVGLQOHSQGEACMWT	LHPASKORSSEKRVGDDLLIVSVATERYLA	180
Db	120	SSSQDKLSPVGLQOHSQGEACMWT	LHPASKORSSEKRVGDDLLIVSVATERYLA	179
Qy	181	ENNEYSIVNASFHVTHMSVOPYGT	GISIMKIVGVYFGDVLRFPFGSDECLTIP	240
Db	180	ENNEYSIVNASFHVTHMSVOPYGT	GISIMKIVGVYFGDVLRFPFGSDECLTIP	239
Qy	241	GQNTVVEGGSVWSQASRLRLRLA	RTPKAGGPIINWHPKIRITITGRVLYGVND	300
Db	240	GQNTVVEGGSVWSQASRLRLRLA	RTPKAGGPIINWHPKIRITITGRVLYGVND	299
Qy	301	LVSEERATTSACVCLAEQEKDOKO	VADLBYGAPITIKYGSTVIVGSHETGLM	360
Db	300	LVSEERATTSACVCLAEQEKDOKO	VADLBYGAPITIKYGSTVIVGSHETGLM	358
Qy	361	KSYETKKKGKGVKAEKQALIHBE	GKMDGLDPSRSGEESRTAIVRKCSLFTK	420
Db	359	KSYETKKKGKGVKAEKQALIHBE	GKMDGLDPSRSGEESRTAIVRKCSLFTK	418
Qy	421	ETLQENRRHGWFPASVNLGEMW	KCLLDLILNYFAQPDMDMEKONFRALRN	480
Db	419	ETLQENRRHGWFPASVNLGEMW	KCLLDLILNYFAQPDMDMEKONFRALRN	478

Qy	481	GGILNLIIEADIXINVTISQGFIAFLAGDESGQWEMISGLYOLIAIIGKNTNCAQ	540
Db	479	EGVNLIEBADIXINITSQGFIAFLADESGQSDLIISTYLIOLIAIIGKNTNCAQ	538
Qy	541	FANSNRLNWLPERLSGQASGSGTGMLDVHJCVLIIDSPALNNMRDEHKVITISLEKIGR	600
Db	539	FANSRLNWLPERLSGQASSEGSMLDVHJCVLIIDSPALNNMRDEHKVITISLEKIGR	598
Qy	601	DPKVLDTVCSJLGVNGVAVRSSQNNICDYLTPGKILLQTAIVDHVSVRENIPIVGRYBG	660
Db	599	DPKVLDTVCSJLGVNGVAVRSSQNNICDYLTPGKILLQTAIVDHVSVIRPNIPIVGRYBG	658
Qy	661	SAVVRKATPEYVMDEHIEKTHMMPHLRIGMATTVGVPRGGGKKMGNGVGDLDYSYGF	720
Db	659	SSMTOKATPEYVMDEHIEKTHMMPHLRIGMATTSGVPRGGGKKMGNGVGDLDYSYGF	718
Qy	721	DGAYLMSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFRGVATSGSPFNULB	780
Db	719	DGAPLMTGGRKTLVVDALPEEPFIRKGDVIGVAILDSVPIIFTNVGVATSGSPFDNLID	778
Qy	781	GMFPFVIVICSSSLCGRFLIGEHGRLYAAPGYEPLYESLLPOOILSLBPCFTYNTSK	840
Db	779	GMFPFVWVSSSSSLCGRFLFGDGHGRLKFAPEWGFSAVOCPLPOOLSLDPCFTYGNLAK	838
Qy	841	RALGAPPLVODDTAVPRPVDTLOTLTPYVQIJDHKLAEHHEMMANMKIISAGMAYDQ	900
Db	839	NVLGAPPLIBDITAVPRKPVDTVTGTVSSVDIOEKLAEHHEMMALNKIISAGMWSGH	898
Qy	901	REDLHKIHPCULVPERLPPAEKRYDIOLAVOTLKTLILAGYISLDPKPAIRNRLPNE	960
Db	899	RDDYHRIHPCULHPEKLPAAEKRYDNOIALVOGLKTLISLGYITMDKPPAIRPRLPNE	958
Qy	961	PPMQSGNYKPAPLDISAVTLTPKMDLYDOLAEHNNHMAKRIIOGQWITYGLANESDMHR	1022
Db	959	IFMQSGNYKPAPLDISAVTLTPKLELDYDOLAEHNNHMAKRIIOGQWITYGLANESBHR	1018
Qy	1021	SPHLVPEYKVDALIKKANRDTSGEVRVTLVYGWMLDPYEGSHALLBASKQONDR	1080
Db	1019	SPHLVPAKVDBALIKKANRDTISSEISANAPGRLTGSSDGRKNGTSGRGTTPQVRLP	1078
Qy	1081	TYRAKRYAVBSGKMYPEFELITAGPMEVGAHADMAPGMLGODENSWAPGDYNEKYU	1140
Db	1079	TYRVERNAVATSGKMYPEFEVLITSGPMEVGMARADCYGAMLGSDSTWAPGHNVTQH	1138
Qy	1141	SGNTSPEKQMAVGVVGVFLDIDIKTISPSLNGELIMDALGSETTPADV--QGNPFLPA	1198
Db	1139	AGSIEHFVARYEAGGVICFIDVKEQITISPSLNGELIMDALGSETTPADVABGVFVPA	1196
Qy	1199	CTLGVGQCARLITYGQDVNTLKFTTCGLOEGVBPCCVMKQDVTHTMYTKDOIPENTEM	1258
Db	1197	CTLGVGQCARLITYGQDVNSLKFETTCGLOEGVBPCCVMKRRVHTMYTKDOIPENTEM	1256
Qy	1259	IDTRIDVTRIPAGSDTPPCLAKISHTPEIMEKANEPLRLSPVICHNEPIDEAEKARY	1318
Db	1257	PDCRIDVTRIPGADTPPHLKISHNTPEIMEKANBPLRLSPVCMGEBPISBQEKARY	1316
Qy	1319	VEIKDROQILKEA-VEAQM-----PAHIDQMSGFTMNDIKGLAHE-DNOBELPSSKM	1378
Db	1317	DEIKROQRLKREKALIAOMOVOTQAAMDHKLKGGFTMMNDIKGLTRNPFDEHADAEMHM	1376
Qy	1372	KRLSPRPRKSGSMTEGVTIONVNNLQPCQVNGMHRSTSEAEWAKYDLCAOGLTPDDKDX	1430
Db	1370	MREGPRPRKSGSLTNTIT---PETMSAALDEMQSTG-----VIDMNGLEBMDDK-K	1428
Qy	1432	RGRSPFKFPRKRGSSSDRAKRSKTDPPSDTVEVSBERGARRENPOIKVSOANORYNG	1490
Db	1430	RGRSPFKFPRKRGSSSDRAKRSKTDPPSDTVEVSBERGARRENPOIKVSOANORYNG	1488
Qy	1492	MNABBSRNLVGSQVGLMATPPTQDRKQMTSTLAQSTVYVGNIEIPABCAKILNERY	1550
Db	1488	AEIPSPV-----PQGPKQLSGSNIQOQVPEVTSGDDEMPABCAKILNERY	1538

QY	1552	GVRIYPGODP	PHVHYIGWTTQOYHL	HSQDNOSK	YKTSVIT	ITDDYDR	VVENWV	OSCMV	1611																																			
QY	1553	GVRIYPGODP	PHVHYIGWTTQOYHL	HSQDNOSK	YKTSVIT	ITDDYDR	VVENWV	OSCMV	1611																																			
Db	1554	GVRIYPGODP	PHVHYIGWTTQOYHL	HSQDNOSK	YKTSVIT	ITDDYDR	VVENWV	OSCMV	1611																																			
QY	1612	RADBLVNEVMA	EAAPAKGASQGM	FIGCSJDS	YTSVGS	PFCEGKDT	SFKYKME	BEKTLPPAI	1671																																			
QY	1672	FVEATSKETI	IOIEIGSATSLPL	SAAVLPS	SDKAVIPQ	PPRLKYOC	LKPHQAR	VPNOS	1731																																			
Db	1654	FVEATSKETI	IOIEIGSATSLPL	SAAVLPS	SDKAVIPQ	PPRLKYOC	LKPHQAR	VPNOS	1731																																			
QY	1732	LOVNAKLSD	IRGSMTCEDAV	NSMLAH	IBEDE	CDILBE	IMDKLS	PSHSHTLYAA	1791																																			
Db	1714	LOVNAKLSD	IRGSMTCEDAV	NSMLAH	IBEDE	CDILBE	IMDKLS	PSHSHTLYAA	1791																																			
QY	1792	LCYOSNRAA	ALCTHNDOKOL	ALAIOSQV	SGELRG	OFYDL	LALHLS	HAATMEACKN	1851																																			
Db	1774	LCYOSNRAA	ALCTHNDOKOL	ALAIOSQV	SGELRG	OFYDL	LALHLS	HAATMEACKN	1851																																			
QY	1852	EFVJPLG	BEKALYEB	BDMGHS	LSRSLQ	TESVRPQ	MKWTDI	-----ABSITE	1897																																			
Db	1834	EYIITPLG	AEKLELY	SDDEMG	HSLSRSL	TESVRPQ	MTETIRP	PIYATSSMP	SVESBPIPD	1893																																		
QY	1898	ISNIVSP	PPPLFV	ARERTM	QALAAV	ETNQV	YHNDP	PVGS	SNHNTPLPLPLK	YDRLLVGM	1957																																	
Db	1894	IDOLYSP	PPPLFV	ARERTM	QALAAV	ETNQV	YHNDP	PVGS	SNHNTPLPLPLK	YDRLLVGM	1953																																	
QY	1958	MRDDEV	KLMTN	PERMTD	SPFDE	KGDE	EHKRG	LHMKMA	GALQ	MCYTLLOH	NDOLR	2017																																
Db	1954	LTDDEVO	RLWMD	PETWDOA	FEBEG	XDEN	HRKGL	TMKMA	GALQ	MCYTLLOH	NDOLR	2013																																
QY	2018	HRVBAIIA	PAHD	PVGD	LOTDQ	LARE	YTEIKOSD	LEPSA	AAKTBRE	FRCPRE	QONNAIISFX	2077																																
Db	2014	HRVBAIIA	PAHD	PVGD	LOTDQ	LARE	YTEIKOSD	LEPSA	AAKTBRE	FRCPRE	QONNAIISFX	2073																																
QY	2078	HLEBED	KENCP	CGSEKL	LARKNE	FPDIT	MAHVS	LALOP	DAENOS	-PEAK	PGAFGLYN	2136																																
Db	2074	NLEBPD	DNOC	CGSEKL	ELGR	LADFP	EDSD	LMOK	SILNALO	BP	PGVEGTA	LEBVTGPTIKYIN	2133																															
QY	2137	IINNVK	LEBE	BAKAI	BBP	PKTPE	KRKYUL	IOITVMA	BSQI	ETPLK	REMS	SLVRO	2196																															
Db	2134	PINVKS	LEBE	BAKAI	BBP	PKTPE	KRKYUL	IOITVMA	BSQI	ETPLK	REMS	SLVRO	2193																															
QY	2197	YDAVGE	LIRALE	KTYVNA	KTKLDVA	EMWVY	LSQIR	ALLP	VONS	OBESE	BLRKLMLYN	2256																																
Db	2194	YDYGEL	VRAL	EKTYVNA	KTKLDVA	EMWVY	LSQIR	ALLP	VONS	OBESE	BLRKLMLYN	2253																																
QY	2257	NHTEF	FOH	DLIRVL	VHENWVA	VMMNTL	IGRR	AOQSDA	OPSSQ	PVAE	-DSKE	KOTSHEM	2314																															
Db	2254	NATPEF	OH	PD	LIRIR	VHENWVA	VMMNTL	IGRR	AOQSDA	-PTQSE	VAGAPS	KEKOTSHEM	2312																															
QY	2315	VVACCR	ELCT	PCRRGR	ONOKAMP	HPFL	LENS	ITILSR	SLRSG	STL	DVA	YSSIMANTE	2374																															
Db	2313	VVACCR	ELCT	PCRRGR	ONOKAMP	HPFL	LENS	ITILSR	SLRSG	STL	DVA	YSSIMANTE	2372																															
QY	2375	LALALRE	HYLEK	LAVUS	RGC	LOSNS	ELVE	KGYD	LD	GM	D	VEGER	YU	PL	FCVW	VAGS	2434																											
Db	2373	LALALRE	HYLEK	LAVUS	RGC	LOSNS	ELVE	KGYD	LD	GM	D	VEGER	YU	PL	FCVW	VAGS	2432																											
QY	2435	VVENAN	VIRLL	IRR	PC	GPAL	RG	EGGL	FR	AI	V	ENRMS	BRIS	DR	CKM	QD	-BAEG	ITA	2493																									
Db	2433	VVENAN	VIRLL	IRR	PC	GPAL	RG	EGGL	FR	AI	V	ENRMS	BRIS	DR	CKM	QD	-BAEG	ITA	2491																									
QY	2494	--NSH	PL	P	S	D	E	D	E	D	I	T	D	G	A	I	N	Y	C	T	L	V	D	L	G	C	A	D	A	G	I	A	L	G	N	E	S	L	R	A	A	I	R	2551
Db	2492	GLNTH	PL	P	S	D	E	D	E	D	I	T	D	G	A	I	N	Y	C	T	L	V	D	L	G	C	A	D	A	G	I	A	L	G	N	E	S	L	R	A	A	I	R	2551
QY	2552	SLVLE	J	O	G	V	L	S	R	P	T	L	N	P	A	G	E	B	P	K	S	D	M	S	G	L																		

Db 2612 YRLBPAFLPDLTATATILKSDGSESDMALANRYGNSILPILIKSGSKFYNEAEVYAST 2671
Qy 2672 LQATHTVRLSKNRLTKGOREAVSDPLVALTSAOPSLKTLKRLTYDVSKSEYTT 2731
Db 2672 LQATHTVRLSKNRLTKGOREAVSDPLVALTSAOPSLKTLKRLTYDVSKSEYTT 2731
Qy 2732 VALRLTLHYERCAKYTGSGAOGAFASDSEKLTVMMLPSNIPDSLKMDYBELFG 2791
Db 2732 VALRLTLHYERCAKYTGSGAOGAFASDSEKLTVMMLPSNIPDSLKMDYBELFG 2791
Qy 2791 KALPCLIAIGCALPPYSLSKNTDBDYGRKMGAP--DQPYMNPIDITNVHLDMDLNS 2848
Db 2852 IYQKSEHYHDMAWASKIRNGWYGGWSOKTHPRLKPYNNMLNDEKERYKPEVRESI 2911
Qy 2849 LVQKSEHYHDMAWASKIRNGWYGGWSOKTHPRLKPYNNMLNDEKERYKPEVRESI 2911
Db 2912 KALLAIGWSEHSEVDIPENNSSMKRQSGRPPPEI--VTDSATPPDYNPVDMTML 2969
Qy 2909 KGLLAIGWSEHSEVDIPENNSSMKRQSGRPPPEI--VTDSATPPDYNPVDMTML 2969
Db 2970 TISREKONMAERLADNADIMAKCKEEL 2998
Qy 2964 TISREKONMAERLADNADIMAKCKEEL 2998
RESULT 2
179144
Partial CDS - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29144
R:Palley, A.; Gactung, S.
Submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid K11C4.
A:Reference number: 220577
A:Accession: T29144
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Release date: 1-5107 <PAU>
A:Cross-references: UNIPROT:Q94279; UNIPARC:UPI00011013D; EMBL:U64854; PIRN:AA818318.1;
A:Experimental source: strain Bristol N2; clone K11C4
C:Gene: CEB-68
A:Map position: 5
A:Introns: 27/1; 64/3; 92/3; 127/1; 158/2; 1222/2; 1300/2; 1347/2; 1391/1; 1419/3; 1517/
3; 3269/2; 3313/2; 3466/1; 3519/3; 3615/3; 3629/3; 3658/2; 3710/1; 3741/3; 3779/2; 3810/
C:Superfamily: Ryanodine receptor; transcritpion initiation factor sigma region 1 homolo

Query Match 43.4%; Score 6828; DB 2; Length 5107;
Best Local Similarity 45.0%; Pred. No. 0;
Matches 1407; Conservative 519; Mismatches 850; Indels 350; Gaps 52;

Qy 113 MYLCLSTSSODKLAFLVGLQHSGBACWMTLHPASRSGEKKRYGDDLLIVSVAT 172
Db 1 MYLCLSTSSODKLAFLVGLQHSGBACWMTLHPASRSGEKKRYGDDLLIVSVAT 60
Qy 173 ERYLHTK---ENEVSI-----VNASPHVTHMSVOPVGTGI 205
Db 61 ERYLHTK---ENEVSI-----VNASPHVTHMSVOPVGTGI 205
Qy 206 SRMKVYGVTEGGDVTFRFGGDECLTIPSTTKDGGONIVTEGGSVMSQASLWLELA 265
Db 121 MTRNMGFLTEGNDVTLFRFGDECLTIPSTTKDGGONIVTEGGSVMSQASLWLELA 180
Qy 266 RTKAGGFLNTPRIRITITGRVYGVNDONEHLYVSEBEATLTSACACLLOEDDDQK 325
Db 181 RTKAGGFLNTPRIRITITGRVYGVNDONEHLYVSEBEATLTSACACLLOEDDDQK 325
Qy 326 VLEDDLEVTGAPITVYGDSTVIVQHSSTGLMISYKSYETKKGGVGVKEKQAILHBEK 385
Db 326 VLEDDLEVTGAPITVYGDSTVIVQHSSTGLMISYKSYETKKGGVGVKEKQAILHBEK 385

Db 240 MLDEKEBGMGNATIRYGETNAFIOHVKTQMLSYQTEVTEYKGLGKVEKKAVALDKGH 299
Qy 386 MODGDLFSRSOEBESRTAVIRKCSLFTKFLNGLETLOENRHSMPFASVNLGEMVCL 445
Db 300 MODCTFFPALBESBSAIVIRKCSVNLKFLGIDALQUBGQSTDMTRVDLNEVTKM 359
Qy 446 EDLINTFAQPDDEMEHEKONKFRALNRQDLFOEBGILNLIJEAIDKINVTISQGFPLG 505
Db 360 EDLIEYFAQPNBQDEKONKFRALNRQDLFOEBGILNLIJEAIDKINVTISQGFPLG 419
Qy 506 FLAQBESQGSWEMISQYQLAAIKGNHTCAQFANSRLNMLFSRLGSAQSGGCTGM 555
Db 420 -LIGETTHKMQISTYLLVLAAMIKGNHTCAQFANSRLNMLFSRLGSAQSGGCTGM 476
Qy 566 LVLHCVLIDSPALNMMDDEHIAKVIISLBEKGRPKYLDVLSLVGNGVAVRSQNN 625
Db 477 LVLHCVLIDSPALNMMDDEHIAKVIISLBEKGRPKYLDVLSLVGNGVAVRSQNN 536
Qy 626 LCVLLPGKULLQTLVADHVSVPNIFVGVGSGAVYRKVFEVMDHIEKTTMMPH 685
Db 587 IYQYLLPGKULLQTLVADHVSVPNIFVGVGSGAVYRKVFEVMDHIEKTTMMPH 596
Qy 688 LRIQMANNTGYTPYGGGKMGANGVGDLYSGYFGAYLMSGGKTPVNRTHASEPYR 745
Db 597 LRIQMANNTGYTPYGGGKMGANGVGDLYSGYFGAYLMSGGKTPVNRTHASEPYR 745
Qy 746 KGLVIGCALDLPVLIINPFGVAVTGSFTNLSGMPFVYSCSKSCRLFGGSEGR 805
Db 652 KGLVIGCALDLPVLIINPFGVAVTGSFTNLSGMPFVYSCSKSCRLFGGSEGR 711
Qy 806 LRYAABEGYSPVLESILPQOLISLEPCFYGNLSKRALAPPLVOD--TAPVTPVDTLQ 864
Db 712 LRYAABEGYSPVLESILPQOLISLEPCFYGNLSKRALAPPLVOD--TAPVTPVDTLQ 864
Qy 865 ITPVYEQKRDKLAENITHEMANAKIKAGMYGQREDLHKHPCLVPEELPAREKY 924
Db 770 ITPVYEQKRDKLAENITHEMANAKIKAGMYGQREDLHKHPCLVPEELPAREKY 829
Qy 925 DIQAVQTLKTLILGYISLIDKPPAIRNVYL--ENEPVQNGYKPAFLDLSAVTLTK 983
Db 830 DIQAVQTLKTLILGYISLIDKPPAIRNVYL--ENEPVQNGYKPAFLDLSAVTLTK 887
Qy 984 MDLVDOLAEHTNMLFEERLQOGWTYGLNE--DSDMERSPHLVYPKYDAIKKANRDT 1041
Db 888 MDLVDOLAEHTNMLFEERLQOGWTYGLNE--DSDMERSPHLVYPKYDAIKKANRDT 947
Qy 1042 ASETVKTLLVGYMLDPYGOHEALLBASQKQADFTTFAEKYAVSSGKTFREPI 1101
Db 948 ASETVKTLLVGYMLDPYGOHEALLBASQKQADFTTFAEKYAVSSGKTFREPI 1006
Qy 1102 LTAGMARGMAHADAPGMMLGODNSMAFQSYNEKYSNGTESFGKQMAAGDVVGYEL 1161
Db 1007 LTAGMARGMAHADAPGMMLGODNSMAFQSYNEKYSNGTESFGKQMAAGDVVGYEL 1065
Qy 1162 DLIDKTIISFSLNGELMDALGETTFADYQ--GDNFVPACTLGVQKALTYGQDVNTLKY 1220
Db 1066 DLIDKTIISFSLNGELMDALGETTFADYQ--GDNFVPACTLGVQKALTYGQDVNTLKY 1125
Qy 1221 FTTGLOSGYEPFCVNMKRDVTHYTKDQPIRENTDEMIDTRI--DVTRIAGSDTPPCIK 1279
Db 1126 FTTGLOSGYEPFCVNMKRDVTHYTKDQPIRENTDEMIDTRI--DVTRIAGSDTPPCIK 1185
Qy 1280 ISHTPFR---MEKANEPLALSLPYCHNEFIDEBK---ARWVEIKDQOOLMGEA 1332
Db 1186 ISHTPFR---MEKANEPLALSLPYCHNEFIDEBK---ARWVEIKDQOOLMGEA 1245
Qy 1333 VEAQMPAHIDQIM--SGFTMNDIKGLAYEDNOEELPSSKMKLPS---RPRKSSMTFG 1387
Db 1246 RAPGIPKPFNDKKEKGLRLSMTGSKDHSDDDRSRKTSNPSQVDDGDEPPA----- 1298
Qy 1388 VTIONYNNLQPGQVNGMERSSEAEAMATYDLGAQGLTPDDKDKRGSRSPKFRS---K 1443
Db 1299 -----VRSILTELPHDBEQIADSNRDLNDR-----HSEKPKGGLSLRLDSNTRK 1346

QY 1256 CGATACAGCAAGCGCGCTGCTATGCGCTGCTTCCGACAACTTCACTACATCTCTG 1315
 DB CTATCCAGAGAGAGCGCGCTGCTATGCGCTGCTTCCGACAACTTCCCTACATGATG 487
 QY 1316 CGAGCATGAGCGGTGATCATCTGCTGCACTGCTACGAGCTGCTGCTGCTGCTGCTG 1375
 DB CAAGCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 547
 QY 1376 AGAATCTGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
 DB AGAATCTGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
 QY 1436 TGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1495
 DB TGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
 QY 1496 CCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1555
 DB CCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
 QY 1556 ACATGCTTACGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1615
 DB ATATGCTTACGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 785
 QY 1616 GGAAG 1675
 DB GGAAG 841
 QY 1676 AGAAG 1735
 DB AGAAG 901
 QY 1736 GGGTGGCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1795
 DB GGGTGGCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
 QY 1796 TCAATGAGACTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1855
 DB TCAATGAGACTTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
 QY 1856 TGGATGATGAG 1915
 DB TGGATGATGAG 1081
 QY 1916 GCGTCAATGAG 1975
 DB GCGTCAATGAG 1141
 QY 1976 AAGGCTGGCGGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2035
 DB AAGGCTGGCGGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201
 QY 2036 TCACTGCGGAGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2095
 DB TCACTGCGGAGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1261
 QY 2096 AGAATCTGCAAG 2155
 DB AGAATCTGCAAG 1321
 QY 2156 TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2215
 DB TGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1391
 QY 2216 AGAAG 2275
 DB AGAAG 1441
 QY 2276 AAGATCTCAACCTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2335
 DB AAGATCTCAACCTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501
 QY 2335 AAGATCTCAACCTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501

QY 2336 TGGCTCACTCAG 2395
 DB TGGCTCACTCAG 1561
 QY 2396 AGAAG 2455
 DB AGAAG 1621
 QY 2456 AGAAG 2515
 DB AGAAG 1681
 QY 2516 TGGCAAGCAATGAG 2575
 DB TGGCAAGCAATGAG 1741
 QY 2576 AATATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2635
 DB AATATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1801
 QY 2636 TGGATGCAATGAG 2695
 DB TGGATGCAATGAG 1861
 QY 2696 AGAAG 2755
 DB AGAAG 1921
 QY 2756 ACGGCAAG 2815
 DB ACGGCAAG 1981
 QY 2816 GGTATTAATGAG 2875
 DB GGTATTAATGAG 2041
 QY 2876 TGGCAAG 2935
 DB TGGCAAG 2101
 QY 2936 GATTCAG 2995
 DB GATTCAG 2161
 QY 2996 CTAAATA 3001
 DB 2162 AAAACA 2167

RESULT 3
 AF009344 866 bp mRNA linear INV 17-APR-2000
 LOCUS
 DEFINITION
 Heliothis virescens ryanodine receptor (rYr) mRNA, partial cds.
 ACCESSION
 AF009344
 VERSION
 AF009344.1 GI:4102114
 KEYWORDS
 SOURCE
 ORGANISM
 Heliothis virescens (tobacco budworm)
 Heliothis virescens
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Noctuidae; Noctuidae; Heliothinae; Heliothis.
 REFERENCE
 1 (bases 1 to 866)
 Puentes, R., Suner, M., Evans, A.D., McCaffery, A.R. and Windasse, J.D.
 Identification of a polymorphic ryanodine receptor gene from
 Heliothis virescens (Lepidoptera: noctuidae)
 Insect Biochem. Mol. Biol. 30 (4), 335-347 (2000)
 JOURNAL
 PUBMED
 10727900
 REFERENCES
 2 (bases 1 to 866)
 Puentes, R. and Windasse, J.D.
 Direct Submission
 Submitted (18-JUN-1997) Biologie et Patologie Diaceutie, INSERM
 U51, Institut Louis Bugnard, CHU Rangueil L3, Toulouse 31403 CEDEX
 04, France

FEATURES		Location/Qualifiers	
source		1..866	
		/organism="Heliobasis virescens"	
		/mol_type="mRNA"	
		/strain="BRC"	
		/db_xref="taxon:7102"	
		/dev_stage="4th and 5th instar larvae"	
		<1..>866	
		/gene="ryr"	
		<1..>866	
		/gene="ryr"	
		/function="intracellular calcium release channel"	
		/note="Ryr; overlaps with AF09345"	
		/codon_start=1	
		/product="ryanodine receptor"	
		/protein_id="AAD01423.1"	
		/db_xref="GI:4102115"	
		/translation="HLKDKDVGFEPTS IAGLANSVLDLDA FERNYAEGLAGLEG AAGERKMHDAEFTCALFRF IOLTCENHLDMONTLRTOAGNTTVNVICVDYLR OESIMDFMYHSHKELIDPAGKANPPKAIIGASOVNTLTVIGPCPNOMAAHBR LMDVVGFLPLFSHMDDLSKSSQVLDKELINLDKMTMLSMLEGNVNETIGK OMDTLVESASVELILKTFDMFLKLDLTSSASFQETDANNQWVLPKPKKXEDQ KSTPEIEIFLLA"	
ORIGIN			
Query Match	27.8%; Score 835.6; DB 2; Length 866;		
Best Local Similarity	97.8%; Pred. No. 26-173;		
Matches 847; Conservative	0; Mismatches 19; Indels 0; Gaps 0;		
QY	1870	CACCTGGAAGACAGAAAGAGCGGCTTCTTACGTCATCGCGGCTCATGACTCC	1929
DB	1	CACCTGGAAGACAGAAAGAGCGGCTTCTTACGTCATCGCGGCTCATGACTCC	60
QY	1930	TGCTCCGCTCGATCTTGAACGCTTGAAGAAACCAAGCTGAAGCTGCGGCGTG	1989
DB	61	TGCTCAGTGTCTGATCTTGAACGCTTGAAGAAACCAAGCTGAAGCTGCGGCGTG	120
QY	1990	GATCTGGAAGAGTGGGCGGAGAGAAACATGATACCGCGAGTTCACCTGCGCATC	2049
DB	121	GATCTGGAAGAGTGGGCGGAGAGAAACATGATACCGAGTTCACCTGCGCATC	180
QY	2050	TTGAGGTTCAATTCAGCTCACTGTAAGACACAACTTGAAGCTGCGAGAACTACCTCGA	2109
DB	181	TTGAGGTTCAATTCAGCTCACTGTAAGACACAACTTGAAGCTGCGAGAACTACCTCGA	240
QY	2110	ACTCAGGCGCGTAACACGACACAGTGAAGTGTGATCTGACCGTCACTACCTGCTG	2169
DB	241	ACTCAGGCGCGTAACACGACACAGTGAAGTGTGATCTGACCGTCACTACCTGCTG	300
QY	2170	CGGCTGCGAGAGTCATCAGGACCTTCTACTGCACTACCAAGAACTGATGAC	2229
DB	301	CGGCTGCGAGAGTCATCAGGACCTTCTACTGCACTACCAAGAACTGATGAC	360
QY	2230	CGGCGCGGCAAGCACTTCTTCAAGGCGATGGCGTCCCAAGTATCAACACC	2289
DB	361	CGGCGCGGCAAGCACTTCTTCAAGGCGATGGCGTCCCAAGTATCAACACC	420
QY	2290	CTCAGTGAAGTCAACAGGACCTTGTACGCAAGATCAGAGGCTTGTGCTCAGG	2349
DB	421	CTCAGTGAAGTCAACAGGACCTTGTACGCAAGATCAGAGGCTTGTGCTCAGG	480
QY	2350	TTGTGGAGGCTGTGGGTGTTCTGTTCTTCTTCCCAATGCAAGAGTGTG	2409
DB	481	TTATGGAGGCTGTGGGTGTTCTGTTCTTCTTCCCAATGCAAGAGTGTG	540
QY	2410	AAGCACTCGTCGAGGTGACCTGTGAAGAACTCCTCAATCGCAAGAGCATGATC	2469
DB	541	AAGCACTCGTCGAGGTGACCTGTGAAGAACTCCTCAATCGCAAGAGCATGATC	600
QY	2470	CCCATGATCTGTGCTTGAAGAAATGTTGTTAATGTTAATCGGCAAGCAATG	2529
DB	601	ACCATGATCTGTGCTTGAAGAAATGTTGTTAATGTTAATCGGCAAGCAATG	660

QY	2530	GTGACACACATGATGATATGCGGCTCCGACAGTGAACCTGATCTGAAATATCTTGACATG	2589
DB	661	GTGACACACATGATGATATGCGGCTCCGACAGTGAACCTGATCTGAAATATCTTGACATG	720
QY	2590	TTTCCTCAAGTGAAGACCTGACCTCGACGCGGCTTCAGAGATGATGATGCAATAC	2649
DB	721	TTTCCTCAAGTGAAGACCTGACCTCGACGCGGCTTCAGAGATGATGATGCAATAC	780
QY	2650	GACGCTGCTGCTGCTCCGACAGTTCAGAGAAATGAAACACAGAGATTATCT	2709
DB	781	GACGCTGCTGCTGCTCCGACAGTTCAGAGAAATGAAACACAGAGATTATCT	840
QY	2710	CCGAGAAATGAGTCTCTCTGAC	2735
DB	841	CCGAGAAATGAGTCTCTCTGAC	866

RESULT 4			
LOCUS	15361 bp	mRNA	linear
DEFINITION	Rabbit skeletal muscle mRNA for ryanodine receptor.		
ACCESSION	X15750		
VERSION	X15750.1	GI:1709	
KEYWORDS	calcium binding protein; channel protein; receptor; ryanodine receptor.		
SOURCE	Oryctolagus cuniculus (rabbit)		
ORGANISM	Oryctolagus cuniculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;		
	Leporidae; Oryctolagus.		
REFERENCE	3 (bases 1 to 15361)		
AUTHORS	Takekoshi, H., Nishimura, S., Matsumoto, T., Ishida, H., Kangawa, K.,		
	Matsumoto, N., Matsuo, H., Ueda, M., Hamaoka, M., Hirose, T. and Numa, S.		
	Primary structure and expression from complementary DNA of skeletal		
	muscle ryanodine receptor		
JOURNAL	Nature 339 (6224), 439-445 (1989)		
PubMed	272567		
REFERENCE	2 (bases 1 to 15361)		
AUTHORS	Takekoshi, H., Nishimura, S., Nishi, M., Ikeda, M. and Sugimoto, T.		
TITLE	A brain-specific transcript from the 3'-terminal region of the		
JOURNAL	skeletal muscle ryanodine receptor gene		
PubMed	FEBS Lett 322 (2), 105-110 (1993)		
REFERENCE	8097730		
AUTHORS	3 (bases 1 to 15361)		
	Numa, S.		
TITLE	Direct Subcloning		
JOURNAL	Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical		
	Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida		
	Sakyo-ku, Kyoto 606, Japan		
COMMENT	*Source: pRR72, pRR203, pRR308, pRR359, pRR451, pRR616. see X15749		
	for ryanodine receptor gene 5' end; X15749 and X15750 seqs are		
	shown as a compiled one in [1]		
	Data kindly reviewed (27-AUG-1989) by Numa S.		
FEATURES			
source			
	1..15361		
	/organism="Oryctolagus cuniculus"		
	/mol_type="mRNA"		
	/db_xref="taxon:9986"		
	/clone="pRR703, pRR256, pRR229, "		
	/issue_type="skeletal muscle"		
	<1..15361		
	/product="ryanodine receptor mRNA"		
	/note="unlabeled protein product; ryanodine receptor (AA		
	1-5037)"		
	/codon_start=1		
	/protein_id="CA33732.1"		
	/db_xref="GI:1710"		
	/db_xref="GOA:P11716"		
	/db_xref="UniProt/SwissProt:P11716"		
	/translation="MGDGGEGEDVOPRTDEVVLCGATVLEKQLCLAAEGFN		
	RLCPLEPTNMGVPPDLAICPTVLEQSLSVRLQBLMTAVTAVGVSSGGGHTLL		
	YGHAILLRHSHRMVLSCLTTRSRSLMDLAIPVGLQEDATGACWTHTPASQRSEGC		